

# Group B Sequences

<b>HPV6b</b>	<b>HPV11</b>
<b>HPV13</b>	<b>HPV34</b>
<b>HPV44</b>	<b>HPV55</b>
<b>HPV64</b>	<b>HPVMM9</b>

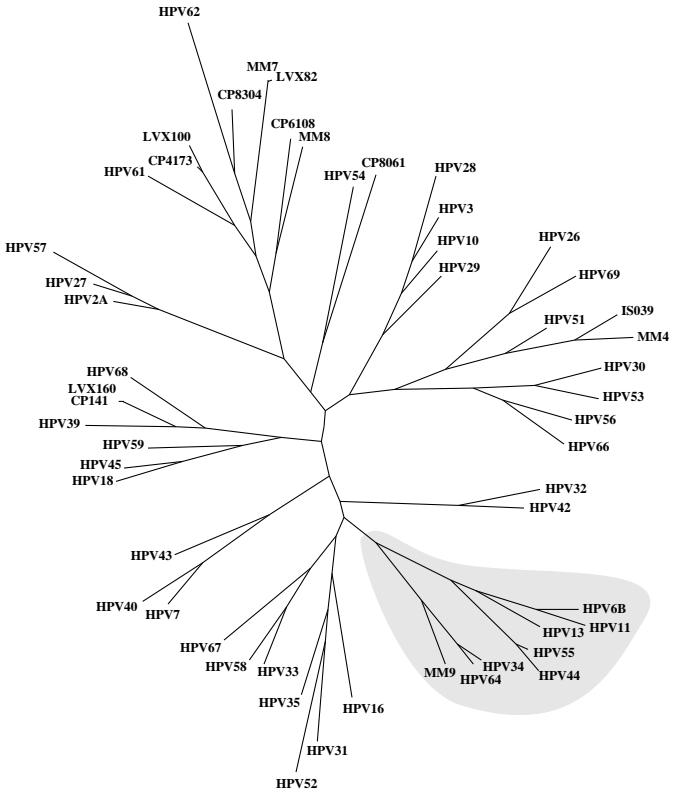
## INTRODUCTION

Group B consists of human papillomavirus types 6b, 11, 13, 34, 44, 55, 64, and the novel virus MM9, a group primarily associated with orogenital lesions with low oncogenic potential. Lorinz et al. classified HPV-6, HPV-11 and HPV-44 as “low risk” viruses [1]. DNA from these three viruses and others in the low-risk class was detected in 20.2% of the low-grade cervical lesions, in 4.2% of the high-grade lesions, and in none of the 153 invasive cancers screened [1].

Many researchers view HPV-6 and HPV-11 together as a functional group [1]. These two viruses are primarily responsible for the benign HPV infection of the anogenital tract. Condylomata acuminata have been shown to harbour HPV-6 or HPV-11 DNA in more than 93% of the cases [1]. Conversely, relatively few HPV-6 and HPV-11 positive genital malignancies have been identified despite extensive international screening. One type of malignancy, although rare, is strongly correlated with HPV-6 and HPV-11 infection: Buschke-Lowenstein tumors, the highly differentiated squamous cell tumors of the genital region, are associated almost exclusively with HPV-6 and HPV-11 [2,3]. HPV-44 and HPV-55, also group B viruses, have been detected in condyloma acuminata of the genital region (vulvar and penile, respectively) [4,5].

The strong association of HPV-6 and HPV-11 with certain types of genital carcinomas appears to be inconsistent with their classification as low-risk. Several explanations have been proposed to explain this anomaly. First, Lorincz et al. suggest the limited number of papillomavirus probes available to researchers may have contributed to the false-positive identification of HPV-6 and HPV-11 [1]. Second, researchers have shown a correlation with oncogenic potential and the presence of a duplicate upstream regulatory region in the genome. A species of HPV-11 with this duplication has been shown to transform baby rat kidney cells and such duplications have been found in carcinomas harbouring HPV-11 and HPV-6 DNA [6–9]. Rubben et al. suggest that cellular and environmental factors following infection may induce this duplication event and/or other rearrangements leading to acquired oncogenic properties [9]. Cofactors which may contribute to malignancy include alcohol and tobacco use and sexual intercourse during menstrual periods [10, 11].

In addition to their involvement with anogenital tract lesions, HPV-6, HPV-11 and HPV-13 are strongly associated with oropharyngeal tract infection. In one study, 72% of all laryngeal papillomas and 25% of all oral papillomas were positive for HPV-6 and HPV-11 DNA [12]. HPV-6 and HPV-11 have been detected in benign papillomas infecting almost every epithelial lining of the upper digestive and respiratory tracts. These tissues include the larynx, sinonasal area, lung, tonsil, tongue, and linings of the oral cavity [6, 12–14]. Unexpectedly, a high percentage (60%) of laryngeal carcinomas have been shown to be positive for HPV-11 DNA [15]. HPV-13, another HPV type highly correlated with oral lesions, was reported by de Villiers to be present in 13% of all oral papillomas [12]. Specifically, HPV-13 has been highly correlated with oral focal epithelial hyperplasia (FEH), a benign lesion situated primarily on the mucosae of the lower lips and cheeks [16]. This disease is frequently found among Indians in Central and South America and in Eskimos



in Greenland and Alaska [16]. However, the prevalence among Caucasians in the same area is much lower [16]. HPV-13 has also been detected in a case of low-grade cervical dysplasia and in Bowenoid papulosis in an HIV-positive male [16].

Several subtypes of HPV-6 have been identified. Subtype 6a has been isolated from tonsillar carcinoma, lung carcinoma and Buschke-Lowenstein tumors [8, 13, 17]. HPV-6b, the prototypical HPV-6 subtype, was initially cloned and sequenced from a benign genital wart [18]. It has been subsequently detected in various genital and upper digestive and respiratory tract lesions. The HPV-6c genome was molecularly cloned from both a respiratory-tract papilloma and a condyloma acuminatum of the cervix [19]. This subtype has also been detected in benign laryngeal papillomas and benign nasopapillomas [20]. The HPV-6d genome, cloned from Buschke-Lowenstein tumors, contains a tandem duplication of 459 base pairs in the noncoding region of the genome [13]. HPV-6e was identified in a genital wart and laryngeal papillomas [19–21]. HPV-6f has been cloned from a benign laryngeal papilloma and a non-inverted nasal papilloma [20, 22]. And, finally, HPV-6vc was cloned from a rapidly growing vulvar verrucous carcinoma [23].

The other viruses in this group, HPV-34, HPV-64, and the novel virus MM9, have been predominantly linked to anogenital lesions. HPV-34 was initially isolated and cloned from a squamous cell carcinoma of Bowen's type and subsequently detected in a genital intraepithelial neoplasia and periungual Bowen's disease [24]. A study which probed lesions with Bowen's disease and squamous cell carcinomas for HPV-34 DNA, reported only one case of positive hybridization, indicating that HPV-34 infection of this nature is relatively rare [24]. HPV-64, a recently identified virus, was cloned and isolated from a vulvar intraepithelial neoplasia [25]. MM9 was derived from a genital swab specimen. Initial prevalence data for MM9 is similar to that obtained for characterized "intermediate-risk" viruses [26].

Of the members of Group B, complete genomic sequences are available for HPV-6b, HPV-11, HPV-13 and HPV-34. HPV-44 has been sequenced over all of E6 and over the My09-My11 fragment of L1, while HPV-55, HPV-64 and the novel variant HPVMM9 have been sequenced only over the latter region. We consider HPV-11 and HPV-6b to be "close types"—sequences which qualify to be distinct types under the criterion of ten percent dissimilarity at the nucleotide level, but between which most of the changes are "silent", causing no difference at the amino acid level (Part III). In addition, the Pygmy Chimpanzee papillomavirus (PCPV-1) is close enough to HPV-13 for these to be considered "close types", although for the purposes of presentation, we have included PCPV-1 in Group I with the other animal papillomaviruses. Although HPV-34 was originally included in Group B on the basis of its association with the rest of the members of this group in the phylogenetic tree used to define the groups, it has since proven to be somewhat problematic in terms of its classification. It seems to cluster with different groups in different analyses, although its association with any group is generally rather weak. For this reason, we chose to exclude HPV-34 from Group B in the context of those analyses that were done "by group". In future it may be prove to be more reasonable to reclassify HPV-34 as a member of Group F, the "catch-all" group; however, we have elected to wait for further evidence before this decision is made. If this turns out to be the case, HPV-64 and HPVMM9 may have to be regrouped as well, since these cluster with HPV-34 on the "group-defining" tree.

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LOCUS HPV6b 7902 bp ds-DNA circular VRL 11-MAR-1994  
 DEFINITION Human papillomavirus type 6b (HPV-6b), complete genome.  
 ACCESSION X00203  
 KEYWORDS complete genome; overlapping genes.  
 SOURCE Human papilloma virus type 6b DNA.  
 REFERENCE 1 (bases 1 to 7902)  
 AUTHORS Schwarz,E., Duerst,M., Demankowski,C., Lattermann,O., Zech,R.,  
 Wolfsperger,E., Suhai,S. and Zur Hausen,H.  
 TITLE DNA sequence and genome organization of genital human  
 papillomavirus type 6b  
 JOURNAL EMBO J. 2, 2341-2348 (1983)  
 COMMENT HPV-11 and HPV-6 are responsible for the large majority of  
 exophytic condylomas in the genital tract. Even though these  
 lesions are frequently present in the genital tract, they are  
 virtually absent in higher grade neoplasias and in cervical  
 cancers. HPV-6 also infects other mucosal types; the respiratory  
 tract, oral cavity and conjunctiva. It has been recovered from  
 approximately 50% of respiratory tract lesions and 50% of all  
 childhood conjunctival papillomas. Respiratory papillomatosis is  
 a rare disease that can be life-threatening because of its  
 recurrent nature and the possibility of obstruction of the airways  
 and respiratory distress. The most frequent sites of infection are  
 the vocal cords in the larynx, but papillomas may also be present  
 in the trachea, lungs, nose and oral cavity. These respiratory  
 papillomas progress to malignancy rarely, as they account for less  
 than 0.1% of all respiratory cancers.

The 7902 bp complete genome of HPV-6b has been cloned in pBR322 and  
 in lambda and was originally recovered from a genital wart. The  
 sense strand has been numbered by comparative analysis with BPV-1  
 and HPV-1a. Both the E6 and E7 ORFs contain conserved Cys-X-X-Cys  
 cysteine doublet motifs. The E6 ORF contains four of these motifs  
 separated by 29, 36 and 29 intervening amino acids, while the E7  
 ORF contains just two separated by 29 amino acids. The E6 ORF also  
 contains a small intron. The E5a ORF codes for a protein of 91  
 amino acids. It has a stretch of 13 amino acids which is very rich  
 in leucine. The L2 ORF contains an extremely conserved cluster of  
 basic residues both at the N terminus and at the C terminus ends.  
 The authors feel that the conserved region of this part of this  
 peptide may interact with the conserved L1 structural peptide,  
 where the variable region may be involved with host or tissue  
 specific functions.

Between the end of L1 and the beginning of E6 lies a small open  
 reading frame E8. The first methionine is located in the middle of  
 the ORF and it has no analog to other papillomaviruses sequenced at  
 the time of publication. In light of these facts, this ORF is  
 probably not functional. Thus, the region from the end of L1 to  
 the beginning of E6 is probably the noncoding region containing the  
 promoter and origin of replication. Within the first segment of  
 this region lies a monotonous repetition of thymine-purine which is  
 just slightly disturbed. Two repeats can be identified within the  
 LCR; a 24 bp tandem repeat and a 9 bp direct repeat. A TATA box is  
 located at position 64 and a cap site is located directly in front  
 of the E6 methionine codon.

BASE COUNT 2438 a 1530 c 1699 g 2235 t  
 ORIGIN

```

1 GTTAATAACA ATCttggttt aaaaaaaTAGg agggaccgaa aacggttcaa ccgaaaacgg
      <- E8 end          E6 orf start ->
      -> CAAT-box <-
(begins at bp 7898)
61 ttgTATATAA accagcccta aaattttagca aacgaggCAT TATGaaaaagt gcaaatgcct
      -> signal           E6 cds ->
                           cap site -> <-
121 ccacgtctgc aacgaccatA Gaccagttgt gcaagacgtt taatcttatct atgcatacgt
  
```

## HPV6b

/\ 3' sj

181 tgc当地ttaa ttgtgtgtt tgcaagaatg cactgaccac agcagagatt tattcatatg  
241 catataaaca cctaaaggc ctgttcgag gcccgtatcc atatgcagcc tgocgtgct  
301 gcctagaatt tcatggaaaa ataaaccaat atagacactt tgattatgct ggatatgcaa  
361 caacagttga agaagaaaact aaacaagaca tcttagacgt gctaattcg gtc当地tca  
421 gtc当地tacc gctgtgTGAa gtggaaaAG Taaaacatat actaaccaag gcccgttca  
E7 orf start -> /\ 5' sj  
481 taaagctaaa ttgtacgtgg aAGggtcgct gc当地tactg ctggacaacA TGcatggaag  
/\ 3' sj E7 cds ->  
541 acatgttacc cTAaggata ttgttattaga cctgcaacct ccagaccctg tagggttaca  
<- E6 end  
601 ttgctatgag caatttagtag acagctcaga agatgaggtg gacgaaagtgg acggacaaga  
661 ttcacaacct taaaacaac atttccaaat agtgc当地tgt tgctgtggat gTGAcagcaa  
E1 orf start ->  
721 cgttcactg gttgtgcagt gtacagaaaac agacatcaga gaagtgcaac agtgc当地tgg  
781 gggaaacacta aacatagtgt gtcccatctg cgc当地tggAG accTAACAac gATGggcggac  
3' sj /\ E1 cds ->  
<- E7 end  
841 gattcaggta cagaaaatga ggggtctggg tgtacaggat ggtttatggt agaagctata  
901 gtgcaacacc caacaggta cacaatatac gacgatgagg atgaggaggt ggaggacagt  
961 gggatgaca ttgtggactt tattgatgac agcaatatta cacacaattc actggaagca  
1021 caggcattgt ttaacaggca ggaggcggac acccattatg cgactgtgca ggacctaaaa  
1081 cgaaagtatt taggtgtcc atatgttagt cctataaaca ctatagccga ggc当地tggaa  
1141 agtgaataaa gtccacgatt ggacgcccatt aaacttacaa gacagccaaa aaaggttaag  
1201 cgacggctgt ttcaaaccag ggaactaacg gacagtggat atggcttattc tgaagtggaa  
1261 gctggaaacgg gaacgc当地tGT agagaaacat ggc当地tccgg aaaatggggg agatggc当地  
5' sj /\  
1321 gaaaaggaca caggaaggga catagagggg gaggaacata cagaggcga agogcccaca  
1381 aacagtgtac gggaggcatgc aggacacgca ggaatattgg aattttaaa atgttaagat  
1441 ttacggc当地t cattacttgg taatgtttaaa gaatgttgg ggctgtctt tatagattt  
1501 attaggccat taaaaggta taaaacaaca tggttagatt ggggtgttagc agggtttgg  
1561 atacatcata gcatatcaga ggc当地tccaa aaattaattt agccattaag tt当地tatgca  
1621 catataacaat ggc当地tccaa tgcatgggg atggatattt tagtattt aagatttt  
1681 gtaataaaaaa gtagaagttc cgttgc当地t acacttgc当地t cgcttataaatacctgaa  
1741 aaccaaatgt taatagagcc accaaaata caaatgtggg ttgc当地tccct gtattgg  
1801 cgtacaggta tatcaaatac gcatgtt ataggggaa caccggaaatg gataacacgc  
1861 caaaatgtt ttaacacgg gttggc当地t agtgc当地tta aatttacaga aatggtgc当地  
1921 tggc当地ttagtataatgacat atgc当地tggg atgtggattt catttataaatacctgaa  
1981 ggagatggg attttaatgc acgacgattt taaaatagca atatgc当地tggg aaaatatgt  
2041 aaagattgtc caactatgtc tagacattt aaacatgc当地t gaaatggaa gatgtctata  
2101 aaacaatggaa taaaacatag gggttctaaa atagaaggca cagggattt gaaaccaatt  
2161 gtacaattcc tacgacatca aataatagaa ttcatccctt ttttaactaa atttaatatt  
2221 tggctgc当地t gtagccaaa aaaaactgc atagccatag taggc当地tcc agatactgg  
2281 aaatcgact ttgttatgg ttaataagg tttctaggag gtacagttt tagtcatgt  
2341 aattccagca gccatttttt gttgc当地tccgg ttagtagat ctaaggtagc attgttagat  
2401 gatgc当地tcc acggatgtt gatataatgt gatacatata tgagaaattt gtttagatgg  
2461 aatccatgtg tatttgc当地t aaaaactgc atagccatag taggc当地tcc agatactgg  
2521 ctatgttgc当地t ccaacataga tattactaaa gaagataat ataagtattt acatactaga  
2581 gtaacaacat ttacattcc aataccattc cttttgaca gaaatggaa tgc当地tggat  
2641 gaaatgtcaa atacaaactg gaaatgtttt ttgaaAGac tgc当地tcaag ccTAGacatt  
E2 orf start ->  
/\ 3' sj  
2701 caggattctg aggacgaggaa agATGgaagc aatagccaaatg cgtttagatg cgtccaggaa  
E2 cds ->  
2761 acagttgtta gaactttaTG Aagaaaacag tactgaccta cacaacatg tattgc当地t  
<- E1 end  
2821 gaaatgc当地t agacatggaa ttgttattt atataaaggca aaacaaatgg gcttgc当地t  
2881 cataggaatg caagttgtc caccataaa ggtgtccggaa gcaaaaaggac ataatgc当地t  
2941 tgaatgtcaa atgc当地ttag aatcattt aaggactgtg tatgtatgg aaccgtgg  
3001 attacaagaa acaagttatg aatgtggca aacaccacccaaacgtt gtttttttt  
3061 gggcaaaaact gtagaagttt aatttgc当地t ctgtc当地tccaaatcata attatgtgg  
3121 atggc当地tggat gtgtatgtgc aggacatga cacctggta aaggtgc当地t gatgtt  
3181 tgc当地tggat atatattaca catgtggaca atttaaaca tattatgtaa actttgTAA  
E4 orf start ->

3241 AGagggcagaa aagtATGgga gcacccaaaca ttgggaagta tgttatggca gcacagttat  
     E4 cds ->  
     /\ 3' sj  
 3301 atgttctcct gcatctgtat ctgcactac acaagaagta tccattcctg aatctactac  
 3361 atacaccccc gcacagaccc ccacccttgt gtcctcaagc accaaggaag acgcagtgca  
 3421 aacgcgcctc agggaaacgag cagcaggagt ccaacagtcc ccttgcacgc ccttgtgtgt  
 3481 ggcccacatt ggacccgtgg acagtgaaaa ccacaacctc atcaactaca atcacgacca  
 3541 gcacccaaaga cggacaaca gtaacagttc agctacgcct aTAGtgaat ttcaagGTga  
     <- E4 end  
     5' sj /\  
 3601 atccaattgt taaaagtgtt ttagatatacg gctaaatgac agacacagac atttatttga  
 3661 tttaatataca tcaacgtggc actgggcctc ctcaaaggca ccacataaac atgcattgt  
 3721 aactgtaaaca tatgatagtg aggaacaaag gcaacagtgg ttagatgtt taaaataacc  
 3781 ccctaccatt agccacaaac tgggatttat gtcactgcac ctattgTAAt ttgtatata  
     <- E2 end  
 3841 gttaaatgtgt aaatatatgg tattgggtGA Atacaactgt acatgtATGg aagtgggtgcc  
     E5a orf start ->      E5a cds ->  
 3901 tgtacaaata gctgcaggaa caaccagcac attcataactg cctgttataa ttgcatttgt  
 3961 tgtatgtttt gtttagcatca tacttattgt atggatatcT GAgtttattg tgtacacatc  
     E5b orf start ->  
 4021 tgtgcttagta ctaacactgc ttttatattt actattgtgg ctgctattaa caacccctt  
 4081 gcaatttttc ctactaactc tacttgtgtg ttactgtccc gcattgtata tacactacta  
 4141 tattgttacc acacagcaAT GAtgctaaca tgtcaattt atgatggaga tacctggctg  
     E5b cds -> <- E5a end  
 4201 ggtttgtgtt tgttatgtgc ctttattgtt gggatgttgg gtttatttattt gatgcactat  
 4261 agagctgtac aaggggataaa acacaccaaa tgtaagaagt gtaacaaaca caactgttaat  
 4321 gatgattatg taactatgca ttatactact gatgggtgatt atatataatat gaatTAGagt  
     <- E5b end  
     L2 orf start ->  
 4381 aaaccgtttt ttatattgtt aacAGtgtat gctttgtata ccATGgcaca tagtagggcc  
     /\ 3' sj      L2 cds ->  
 4441 cgacgacgc a gctgcgc tc agctacacag ctatataaaa catgtaaaact cactggaca  
 4501 tgccccccag atgttaattcc taaggtggag cacaacacca ttgcagatca aatATTAAAA  
     signal ->  
 4561 tggggaaattt tgggggtgtt ttttgggggg ttgggtatacg gcacgggttc cggcactgg  
 4621 ggtcgactg gctatgtcc cttacaaaact tctgcaaaac cttctattac tagtggccct  
 4681 atggctcgtc ctctgtgtt ggtggaccc tggccccc cggatccatc tattgtgtct  
 4741 ttaatttgaag aatccggcaat cattaacgc ggggcgcctg aaatttgcc ccctgcacac  
 4801 ggtgggttta caattacatc ctctgaaaaca actaccctg caatatttga tgatcatgtt  
 4861 actagtcaca ctactactag tatattttaga aatccgtct ttacagaacc ttctgtaaaca  
 4921 caaccccaac cacccgtgaa ggctaatttgc catatattaa ttctgcacc cactgtaaacg  
 4981 tcacacccta tagagggaaat tccttttagat acttttggg tatcatctag tgatagcggt  
 5041 cctacatcca gtacccctgt tcctgttact gcacccgc ctcgtgtgg cctatata  
 5101 cgtgcattgc accagggtca gtttacagac cctgcatttc ttccactcc tcaacgctt  
 5161 attacatatg ataaccctgt atatgtttttt gggatgtt ggttacaatt tagtcatgtat  
 5221 tctatacaca atgcacccgtt gggatgtt gtttgcataa ttgcgttgc cagacccgc  
 5281 attgcgtccc gacgtggcc tggccgttact agtgcgtt gacaacgggg gtctatgcac  
 5341 actcgacgc gaaagcacat agggggccgc attcattttt tttatgtat ttccaccc  
 5401 gcacaggctg cagaagaaat agaaatgcac cctcttgcg ctgcacagga tgatacattt  
 5461 gatattttagt ctgaatcttt tgaacctggc attaacccta cccaaacaccc tggtaacaaat  
 5521 atatcagata cataatttacatc ttccacaccc aatacgtt cacaacccgtt gggtaacacc  
 5581 acagttccat tggcacttcc taatgaccc tttttacaat ctggccctga tataactttt  
 5641 cctactgcac ctatggaaac acccttttagt cctgtAAActc ctgccttacc tacaggcc  
     L1 orf start ->  
 5701 gttttcatta caggttctgg attttatttg catccgtat ggttatttgc acgttaacgc  
 5761 cgttaaacgtt ttccttattt ttttcAGAT GtggccggccT AGcgacagca cagttatgt  
     L1 cds ->      <- L2 end  
     /\ 3' sj  
 5821 gcctcctcctt aaccctgtat ccaaaagggt tgccacggat gcttattgtt ctcgcaccaa  
 5881 catattttat catgccagca gttctgact tcttgcgtt ggacatccat attttccat  
 5941 aaaacgggc aacaaaactg ttgtgcacca ggtgtcaggat tatcaataca gggatattaa  
 6001 ggtgggttta ccagatccat acaaatttgc attgcctgac tcgtctctt tcgatccac  
 6061 aacacaacgt ttagtatggg catgcacagg ccttagggat ggcaggggac agccattagg  
 6121 tgtgggtgtt agtggacatc ctttccaaa taaatatgtt gatgttggaaa attcaggag

HPV6b

LOCUS HPV11 7931 bp ds-DNA circular VRL 30-SEP-1988  
 DEFINITION Human papillomavirus type 11 (HPV-11), complete genome.  
 ACCESSION M14119  
 SOURCE Human laryngeal papillomavirus type 11 DNA recovered from a laryngeal papilloma.  
 REFERENCE 1 (bases 1 to 7931)  
 AUTHORS Dartmann,K., Schwarz,E., Gissmann,L. and Zur Hausen,H.  
 TITLE The nucleotide sequence and genome organization of human papilloma virus type 11  
 JOURNAL Virology 151, 124-130 (1986)  
 COMMENT HPV-11 and HPV-6 are responsible for the large majority of exophytic condylomas in the genital tract. Even though these lesions are frequently present in the genital tract, they are virtually absent in higher grade neoplasias and in cervical cancers. HPV-11 also infects other mucosal types; the respiratory tract, oral cavity and conjunctiva. It has been recovered from approximately 50% of respiratory tract lesions and 50% of all childhood conjunctival papillomas. Respiratory papillomatosis is a rare disease that can be life-threatening because of its recurrent nature and the possibility of obstruction of the airways and respiratory distress. The most frequent sites of infection are the vocal cords in the larynx, but papillomas may also be present in the trachea, lungs, nose and oral cavity. These respiratory papillomas progress to malignancy rarely, as they account for less than 0.1% of all respiratory cancers.

The complete genome of HPV11 was cloned from the laryngeal papilloma of a 15-year-old patient. The sense strand, containing all ORF's of significant length, is shown, with the first position of the circular genome defined by alignment to HPV6b. Designation of early and late ORF's is based on homology with HPV6b, to which it is 82% similar at the nucleotide level. A TATA box is shown 36 bp upstream from the beginning of the E6 cds and a corresponding CAAT box is found 57 bp upstream from the TATA box.

Polyadenylation signals can be found mostly following the late coding regions. A 12-bp-long palindromic sequence responsible for binding of the E2 protein can be found repeated four times in the non-coding LCR region between L1 and E6. Also housed in the LCR are several short direct repeats that are up to 16 bp in length. The authors also note that the first 200 nucleotides of the LCR has an unusually high T content (53%) and an unusually low C content (2%).

BASE COUNT 2406 a 1519 c 1736 g 2270 t  
 ORIGIN 4557 bp upstream of HindIII site; 101 bp upstream from beginning of E6 cds  
 1 cttataaaCA ATCTTAGTTT AAAAaagagg agggACGAA AACGGTtcaA CCGAAAACGG  
 signal -> -> signal -> E2 bind -> E2 bind  
 E6 orf start ->  
 61 TtataATATAA Accagcccaa aaaatttagca gacgaggcat tATGaaaagt aaagatgcct  
 signal -> <- E6 cds ->  
 121 ccacgtctgc aacatctata gaccagttgt gcaagacgtt taatcttct ttgcacactc  
 181 tgcaaattca gtgcgtgtt tgcaggaatg cactgaccac cgcagagata tatgcatatg  
 241 cctataagaa cctaaagggtt gtgtggcgag acaactttcc ctttgacgcg tgcgcgtt  
 301 gcttagaact gcaaggaaaa attaacaat atagacactt taattatgct gcatatgcac  
 361 ctacagtaga agaagaaaa acc aatgaagata ttttaaaagt gttaaatcggt tgcgcgtt  
 421 gtcacaagcc gttgtgtgaa atagaaaaac taaagcacat attggaaag gcacgcgttca  
 481 taaaactaaa TAAccagtgg aagggtcggt gcttacactg ctggacaacA TGcatggaaag  
 E7 orf start -> E7 cds ->  
 541 acttgttacc cTAAGgata tagtactaga cctgcagcct cctgaccctg tagggttaca  
 <- E6 end  
 601 ttgctatgag caatttagaa acagctcaga agatgagggt gacaagggtgg acaaacaaga  
 661 cgcacaacct ttaacacaac attaccaaattt actgacctgt tgctgtggat gTGAcagcaa  
 E1 orf start ->  
 721 cgtccgactg gttgtggagt gcacagacgg agacatcaga caactacaag acctttgct

HPV11



## HPV11

7141 gtttccccctt ggacgtaagt ttttattgca aagtggatat cgaggacgga cgtctgctcg  
7201 tacaggtata aagcgcggcag ctgtgtctaa gccctctaca gcccccaaac gaaaacgtac  
7261 caaaacccaaa aagTAAAtata tgtgtgtcag tgtgttgtt tatttatatg ttgttgttagT  
    <- L1 end  repeat region start ->  
7321 GTGTATATGT TTcttgtaTT GTGTATATGT GTATATGTTT GTGTATATGT GTATGTTATG  
7381 TATGTTatgt TGTATGTAT GTTtgtgtgt ttagtgtgtg tatatatgg tggaaatgtgt  
    repeat region end <-  
7441 atgtatgttt ttgtgcAATA AAcaattatt atgtgtgtcc tgttacaccc agtactaag  
    signal -> <-  
7501 ttgttttg caggcgccgt ttgtgttgcc ttcatattat attatatata tttgtaatat  
7561 acctatacta tgttacccccc ccccacttgc aACCGTTTC GGTtgccctt acatacactt  
    -> E2 bind  
7621 acctcaaatt tttataacg ttgtttgtac taatccata ttttgtgtgc caaggtacat  
7681 attgcctgc caagtatctt gccaacaaca cacctggcca gggcgccgtt ttgcattgact  
7741 aatgtacAAT AAAcctgtcg ttgttacaa ttgttgtgat tgcaggccaa ggtaaaagc  
    signal ->  
7801 attttggct tctagctgaa cattttgtat cccttagtat attatgcaca atacccacaa  
7861 aatgagtaac ctaaggtcac acacctgcaA CCGGTTTCGG Ttaccacac cctacatatt  
    -> E2 bind  
7921 tccttcttat a

LOCUS HPV13 7880 bp ds-DNA VRL 01-DEC-1992  
 DEFINITION Human papilloma virus type 13 (HPV-13), complete genome.  
 ACCESSION X62843  
 KEYWORDS genome.  
 SOURCE Human papillomavirus type 13 DNA recovered from FEH lesions from a 13 year old Turkish girl.  
 REFERENCE 1 (bases 1 to 7880)  
 AUTHORS Van Ranst,M., Fuse,A., Fiten,P., Beuken,E., Pfister,H., Burk,R.D. and Opdenakker,G.  
 TITLE Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparison of the genome organizations  
 JOURNAL Virology 190, 587-596 (1992)  
 COMMENT HPV13 belongs to a subgroup of orogenital papillomaviruses (including also HPV6, HPV11, HPV43, HPV44) associated as a group with benign orogenital lesions (FEH, condyloma acuminata and low-grade cervical neoplasia), and only rarely with cervical cancer. In addition to its similarity to other HPVs, HPV-13 has been shown to be 85% similar to a pigmy chimpanzee papillomavirus (PCPV-1) cloned from a colony of pigmy chimpanzees afflicted by a FEH-like disease. Van Ranst et al. contend that this close relationship indicates the possibility of cross-species transmission.

HPV13 itself is strongly associated with oral focal epithelial hyperplasia (FEH). FEH is characterized by multiple and discrete nodular elevations of the oral mucosa. Its prevalence is high in Indians in Central and South America and in Eskimos in Greenland and Alaska, but is low in Caucasians who live in the same area. Recently, HPV-13 has been detected by PCR in a case of low-grade cervical dysplasia and by *in situ* hybridization in Bowenoid papulosis in an HIV-positive male. In both of these instances, HPV16 was also present in the lesion. Van Ranst et al. contend that the discovery of HPV13 in these recent cases along with the relative rarity of FEH in the Caucasian population to which the subjects belonged may point to the existence of a hidden reservoir of virus in this population.

The complete genome of HPV-13 was cloned from the FEH lesions of a 13-year-old Turkish girl. The sense strand, containing all ORF's of significant length, is shown, with the first position of the circular genome defined by homology with HPV6 and HPV11. The E6 ORF of HPV-13 contains four copies of the cysteine doublet motif. This protein may be involved with the binding of p53. Also this ORF, as is the case with types 6, 11, and 44, does not contain the splice acceptor/donor pair which seems to be critical for E7 expression. The E7 ORF of HPV-13 contains a degenerate form of the cell division motif which may mediate binding of the tumor suppressor protein pRB-105. In the beginning of the E2 ORF, HPV-13 contains a putative leucine zipper motif. This motif has been found to be degenerate in the high-risk papillomaviruses. It has been speculated that this motif could mediate the binding of the E2 activator to the URR, which blocks transcription of E6.

The upstream regulatory region (URR) contains several promoter elements and transcription factors: TATA box at nt 68, CAAT signal at nt 9, 5 NF-1 binding sites at 7587, 7607, 7717, 7741, and 7761, 2 AP-1 binding sites at 7404 and 7810, Oct-1 binding site at 7324, and 4 copies of the E2 binding region. Unlike many other genital papillomaviruses, HPV-13 does not house a glucocorticoid response element. Thus, van Ranst et al. believe it may not be influenced by steroid hormones.

BASE COUNT 2452 a 1480 c 1628 g 2320 t  
 ORIGIN degenerate HpaI site; 103 bp upstream from beginning of E6 cds  
 1 gtttctaaCA ATCTtaagtt taaaaatag gtgggACCGA AAACGGTttT AACCGAAAAC  
 signal -> E6 orf start ->

HPV13



# HPV13

6481 tgcggaaagga acaaattgtt gcaaggcatt tcttaacag ggcaggctct gttggtaac  
 6541 aaatcccagc agaattataat gttaagggtt gtaataact ttctaatagt atttactata  
 6601 tactcccg tggctctt ggtcttctg aggcccatgtt gtttAATAAA ccttatttggt  
signal ->  
 6661 tacaaaaggc ccagggacac aataatggta tatgttggg caatcacttg tttgttactg  
 6721 tagttgatac tacacgcagt actaacatga ctgtgtgtc agccactaca tcatctctt  
 6781 cagacacata taagggccaca gaatataaac agtacatgcg acatgttagaa gaattttgatt  
 6841 tacaatttat ttcttcaattt tgcaacttta aattaactgc agaggtttagt tcatatattt  
 6901 atactatgaa ttcttcaattt cttagaactg ggaactttgg gctatctccc ctttcctaattt  
 6961 gaacattaga agacacatattt agatatgtac aatctcaggc cataacgtgt caaaaggcata  
 7021 cactgttata agaaaaaacag gatccgtatg cgggtttagt tttttgggag gttatctta  
 7181 agggaaaagtt ttcttagtggaa ctatagtcgtt atcccccttgg cagaaaaatttt ttatcacaa  
 7141 caggcgttca gtcttagtggcc ccttatttcgtt taggttaggaa acgtgtgtca ttcatatctt  
 7201 ctgccacacc tactacacgt aaaaaagcta aaaggaaaTA Atagttgtt tatgatttgt  
-< L1 end  
 7261 tatgtatgtc acgtttgttt gtactgtatg tatgttgggt actgtatgtg taatgttgg  
 7321 tggatGTGCA Tgttactttat taaagaatgt gtgtgtgtgt ttgtatgcAA TAAAAtctaat  
-> potential Oct-1 bind signal ->  
 7381 ctgtgggtc ctgttccacc ctatGAGTAA gtggatgtt gtgtctcggt tgggtttttt  
putative AP-1 bind ->  
 7441 tataactatac tataacatttta gtgcaaccat ttgttaactt ttcttacattt ttacgtctcc  
 7501 atattaagtg caACCGATT CGGTtgctat tgtttgcg accgatttgg tgcagcgcac  
E2 bind ->  
 7561 tggatgtatata atcttaccta ccgccttGCCA AAattatcca ccgttGCCA AAatcacccca  
NF1 -> NF-1 ->  
 7621 cacacctggc gttgttaggg cgccgttata tatattttactt aaatcttactt aatctttctt  
 7681 tcactcattt tacctttata acaataacttt tgctttCAA GTacatTTT gtacttacta  
NF-1 ->  
 7741 GCCAAATgcct gaaagggttt TTGGCTacca gcactacatt tttgtacagt taatgttaca  
NF-1 -> NF-1 ->  
 7801 tgtataaaaaT GAGTAACcta aggtcacacaca cctgcaaACC GGTATCGGTt aaaaacacacc  
-> <- E2 binding -> <-  
putative AP-1 binding  
 7861 ctctatagtt ctttataattt

LOCUS HPV34 7723 bp ds-DNA VRL 04-OCT-1993  
 DEFINITION Human papillomavirus type 34 (HPV-34), complete genome.  
 ACCESSION X74476  
 SOURCE Human papillomavirus type 34 DNA.  
 REFERENCE 1 (bases 1 to 7723)  
 AUTHORS Delius,H. and Hofmann,B.  
 TITLE Primer-directed sequencing of human papillomavirus types  
 JOURNAL Curr. Top. Microbiol. Immunol. 186, 13-31 (1994)  
 REFERENCE 2 (bases 1 to 7723)  
 AUTHORS Delius,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-AUG-1993) to the EMBL/GenBank/DDBJ databases. H.  
 Delius, Deutsches Krebsforschungszentrum, Abteilung ATV, Im  
 Neuenheimer Feld 506, W 6900 Heidelberg, FRG  
 COMMENT HPV-34 belongs to a group primarily associated with orogenital  
 lesions with low oncogenic potential. HPV-34 was initially  
 isolated and cloned from a squamous cell carcinoma of Bowen's  
 type in 1986 by Kawashima et al. (J. Virol. 57:688-92)  
 and subsequently has been sequenced by Dr. H. Delius. It has  
 also been detected in a genital intraepithelial  
 neoplasia and periungual Bowen's disease. A study which probed  
 lesions with Bowen's disease and squamous cell carcinomas for  
 HPV-34 DNA, reported only one case of positive hybridization,  
 indicating that HPV-34 infection of this nature is relatively  
 rare (Kawashima et al. J Virol 57: 688-92 (1986)).  
  
 BASE COUNT 2475 a 1339 c 1614 g 2295 t  
 ORIGIN 101 bp upstream from beginning of E6 cds  
 1 actataatcc tactataaaa tatagggtgT AACCGAAAC GGTTgcaACC GATATCGGTg  
     E6 orf start ->  
     E2 bind ->      E2 bind ->  
 61 catatataag tgctgcagta cactgctgga cagattggga aATGttttt cccaatcctg  
     E6 cds ->  
 121 aggaacggcc atacaagcta ccagccttat gtgaagaggt caacattca atacatgaaa  
 181 tagaatttggta ctgtgtgtat tgcgaaacgac aactgtacag atgtgaggtat tatgatttt  
 241 tatttagaga ttatgtgttt gtatataaaaa agggaaACC ACTTGGGGTa tgtaaccgt  
     E2 bind ->  
 301 gtttactgtt ttactcaaag gtttagacaat atagaagata taaccaatca gtgtatggac  
 361 ggacgtttaga gaatttaact aacaaacagt tttgttaat tttataagg tgccggaaat  
 421 gccaaaaacc actgtgttcca ttggaaaaaggc aaaggcatgt agaTGAAaac aaacggttc  
     E7 orf start ->  
 481 accaaatagc ggatcagtgg accggacgt gtacacagt ctggagacca tctgcaacag  
 541 tgggtAAAgA ATGcatggaa aaaaaccaag tttgtgttag atctgaaacc  
     E7 cds ->  
     <- E6 end  
 601 aacgaccgag actgACCTTA CATGTTacga gtcattagac aactcagagg atgaggatga  
     E2 bind ->  
 661 aacagacagc catctagaaa gacaagctga gcaagcctgg tacagaatag ttactgtatt  
 721 cagcagatgt cagtcacag tttgttctac cattgagac acacacgttg acctatttagt  
 781 gtttagaagac ctgttatgg gtgcactaaaa aatttgtgtc cccaaactgtt ccagacgc  
 841 aTAAcagaag ATGgctgatt caggtaattt ggaagggagg tttttttttt gtttaatgt  
     E1 cds ->  
 E1 orf start ->  
     <- E7 end  
 901 agaaggccatt gtagaaagga aaacagggga tgcaataccca gcagatgaaa attatgtgg  
 961 ggacgataca gaggattctg aatgggggaa ttttattgtt aatgcacaca tatctaataat  
 1021 atattccacag cagaaatttgc acacgatccatatactca cagcaatgtt atgcagacaa  
 1081 tgaggctata cgtgttctaa aacggaaatgt tgccggatgt gctggcgtt gcccacac  
 1141 taaaagacat gaattgttgc aacaaacagcg tagtccatgtt atattgtgtca taagggac  
 1201 taatactaca tctacacacc tattgtgtca ggaacaagac agcggatgtt gcaataactgt  
 1261 agtggaaacgc tacggagac aggttacccggg gcccggggggaa tttttttttt gttttttt  
 1321 tagtaacaac ggcagccaaa tggcgatcgcc agggggaaaca aatgtgggtt ccagtagcat  
 1381 ttcaaatatgt gatataaaaa tggaaagcac acctataacg gacattacaa acatattaaa  
 1441 aagtagtaat gtaaggcaaa cattattacg aaaattttttt gaggatataatgtt gattaatgt  
 1501 tatggaaatgtt gtaaggccctt ataaaatgtt gttttttttt gttttttttt gttttttttt

## HPV34

1561 agtgtttggg gtagcgccat cattggcaga aagttaaaa tcattactaa cccaatattg  
1621 cctatacata catctacaat gttAACATG ttCGTGGGT ataATAGTAT tATTGTTAGC  
1681 aagATTAAG tgcaataaaa atAGATTGAC agTACAaaaa TTATTACATG ggTTATTAAGA  
1741 tgtaacacag gaatatATGT taatAGAACCC acCTAGACTA agAACGACGC catGTGCATT  
1801 atactggTC agaactAGCC tatcaaACAT tagtgAAACG gtgggAGAAG tacCCGAATG  
1861 gattAAAAGA caaacAGTAG tacAGCACAG cttagAGGAC tGTCAATTG acCTATCTCA  
1921 aatGGTACAG tggcATTG ATAATGACAT aacaATGAC tGTGAATAG catATAATA  
1981 tgcattATTA GcatCTGAGG ATAGCAATGC tGCTGCATT TAAAAAGCA atGCACAAAGC  
2041 AAAATATGTT aaggATTGtg GAACAATGTG TAGACATTA AAAGCTGCAG aAGTAAACA  
2101 aatGACTATG TCACAAATGGA TTACACATAG ATGTGATTA ATAGATGATG gAGGAAACTG  
2161 gaaACATATTG GTGCAATTG TAAGATATCA GCAGGTTGAA TTTGTACCGT TTTAATTG  
2221 TTTAAACAA TTTTAAAGG GTATCACC AAACAAATGT ATAGTTATAT ATGGACCAC  
2281 agatacAGGA aAGTCACATT ttGGAATGAG TTAATGCAG TTTATGCAG gtGTTGTT  
2341 ttcATATGTA aATTCCAATA GTCATTTTG GTTATGCCA TTGGCTGATG cAAAAATGGC  
2401 attATTAGAT gATGCAACAC CTGCACTGCTG GACATATATT GATAGATATT TAAGAAATGC  
2461 attAGATGGC aATCCTATGT GTTGAACAGG AAAACATAAA CATTATTAC AAATTAAATG  
2521 tcCTCCATTA CTAATAACAT CAAATAACAA TCCATAAGCA GATGATACCT GGAATATT  
2581 gcACAGTGA ATGAAAGTGT TTACGTTTC AAATCCATT CCATTGACA GTAATGGAAA  
2641 tccACTATAC CAACTTACTA ATGAAAACGTG GAAGGCATT TTTACAAAGA CGTGGTCAA  
2701 actAGATTAA ACAGAGGACG ACGACAAGGA aaATGATGGA GACACTGTGC AAACGTTAA  
E2 orf start -> E2 cds ->  
2761 gtgcgtgtca ggacgcaatc ctagaactgt aTGAacgtga tagtatacat ttaagtgtatc  
<- E1 end  
2821 atattgtatca ctggAAACAC gtgcgactgg AAAATGTATT ATTACATAAG gcacgtgaaa  
2881 tgggactgca atcaGTTAAC caacaAGCGG tgccaAGCCT tgcagtatca cgatccaaAG  
2941 ggcataatgc aattGAACTA caattAGCCC tagAAAGTTT AATGAATCA AGTATAACAA  
3001 cagaAGAATG gacattACAA cagacaAGGT gggAACAGTG ggtAACCGGAC ccaAAACAAAT  
3061 gTTTAAAGG AGTGGAAAAA ACAGTAGAAAG TTAGATATGA CTGTGACAAG GACAACACCA  
3121 tgcaatATGT ggtatGGACA TTTGTGTATT ATTGGTTGGA AGGCAAGTGG TATAAAGTGA  
3181 gtagccatGT agatTATAAT ggtatATATT ATGAAACACA GGACAATGAA AAGGTATATT  
3241 atacacaATT tgacAGAGAT GCAAAACGAT ATGGGGTTAA AGGAATATGG GATGTATGTA  
3301 tggccgtaa ggTAAATATGT TTTGCTCCTG TATTTAGCCC gtgtGAAGTA tcoactcctg  
E4 orf start ->  
NH<sub>2</sub> terminus unknown  
3361 aaATTGTTAG ACCCCTGCAC ACAAGCAACA GCAAGCAACGC ACAGGACGCG GGTGTGCCAA  
3421 cacggAAACG GCAAGACAGAG TGTAACCCAG ACAGGGGGCC CTTGGACTTT GTACATAACC  
3481 tacAGCCCAC AACAGACTCA TCGACCCAGT GTACTCTACA TAATGTTGCG CCAAATAGTAC  
<- E4 end  
3541 attTTAAAGG tgacAAAAAC AGTTAAAAT GCTTAAGATA TAGGATGCA TAAAGGGTATT  
3601 cacATTGTT TAATAATGTA ACAACTACAT GGCATTGGAC CAATAATACA AATAGTAAAT  
3661 gtggGTGTAAT tacATTTATG TTTCCAGTA CATCCCAACA AAAACAATTt TTACAATGTG



HPV34

LOCUS HPV44E6 590 bp ds-DNA VRL 15-SEP-1989  
 DEFINITION Human papillomavirus type 44 (HPV-44), E6 region.  
 ACCESSION M27023  
 SOURCE Human papillomavirus type 44 DNA recovered from a vulvar condyloma.  
 REFERENCE 1 (bases 1 to 590)  
 AUTHORS Lorincz,A.T., Quinn,A.P., Goldsborough,M.D., Schmidt,B.J. and Temple,G.F.  
 TITLE Cloning and partial DNA sequencing of two new human papillomavirus types associated with condylomas and low-grade cervical neoplasia  
 JOURNAL J. Virol. 63, 2829-2834 (1989)  
 COMMENT HPV-44 is a mucosatropic HPV which to date has not been detected in cervical cancer. Prevalence studies indicate that HPV-44 and HPV-43 have been found in 4% of cervical intraepithelial neoplasms, but in none of the 56 cervical cancers tested.

During the analysis of approximately 1000 anogenital tissue samples, two new HPV types, HPV-43 and HPV-44, were identified. The complete genome of HPV-44 was recovered from a vulvar condyloma and cloned into bacteriophage lambda. The biopsy was taken from a woman from the Detroit Michigan area. The DNA recovered was a single 7.8 kb BamHI fragment. Only the E6 region of the cloned sample has been sequenced, although the positions of the ORFs for the entire genome have been deduced and are consistent with the organization of DNA from HPV-6b. A possible feature of HPV types associated with malignant lesions is the potential to produce a different E6 protein by alternative splicing. This potential has been found in types HPV-16, HPV-18, and HPV-31. HPV-44 has a potential E6 splice donor at nt 229, but does not contain a potential splice acceptor.

BASE COUNT 197 a 117 c 124 g 152 t  
 ORIGIN 102 bp upstream from beginning of E6 cds  
 1 aataataatc taacctttac aaaaaagagg aggaACCGAA TTCGGTtcca ACCGAAAACG  
 E2 bind -> E2 bind ->  
 61 GTtataTAAa aaccagccca aaaattaagc aagcggggca taATGaaag tgcaaatgcc  
 E6 orf start -> E6 cds ->  
 121 tccacgtctg cacaaggat agaccagtgc tgcaaggagt gcaacattcc tatgcacaat  
 181 ctgcaaattt tatgcgtgtt ttgcagaaaa acgttaagta ctgcagaggt ttattcattc  
 241 gcatataaac agttatatgt agtgtaccga ggaaacttgc catttgccgc ctgtgccatt  
 301 tgtttagaaac tacaaggtaa ggtcaatcaa tttaggcatt ttaactacgc gggatatgca  
 361 gtaacagtgg aagaagaaac aaataagtca attctggacg tgctgatacg ctgtatattg  
 421 tgccacaaac cattgtgcca cgtggaaaag gtgcgccaca tattggacaa ggcgcgattc  
 481 attaaattac aagatACCTG GAAGGGTcgc tgcttccatt gttggacatc atgcatggaa  
 E2 bind ->  
 541 actataactac ctTAAaggaa attgtttac agctggaaacc tcctgaccct  
 <- E6 end

//

HPV44MY911

LOCUS HPV55MY911 455 bp ds-DNA VRL 16-OCT-1994  
 DEFINITION Human papillomavirus type 55 (HPV-55), partial L1 cds, My09/My11  
 region.  
 ACCESSION U12494  
 SOURCE Human papillomavirus type 55 DNA.  
 REFERENCE 1 (bases 1 to 455)  
 AUTHORS Bernard,H.-U., Chan,S.-Y., Manos,M.M., Ong,C.-K., Villa,L.L.,  
 Delius,H., Peyton,C.L., Bauer,H.M., and Wheeler,C.M.  
 TITLE Identification and assessment of known and novel human  
 papillomaviruses by PCR amplification, restriction fragment  
 length polymorphisms, nucleotide sequence, and phylogenetic  
 algorithms  
 JOURNAL J. Infect. Dis. (1994) In press  
 COMMENT HPV-55 was first isolated from a penile condyloma acuminata.  
 Cloned HPV-55 DNA was obtained from the Papillomavirus Reference  
 Center, Heidelberg and subsequently sequenced by Dr. H. Delius  
 over the L1 MY09/MY11 segment. HPV-55 and the several other HPV  
 types recently sequenced over the MY09/MY11 primer region by Dr.  
 Delius were used as type-specific probes to screen DNA for novel  
 genital HPV types. The screened DNA was obtained from four recent  
 epidemiological studies. Primer regions are annotated in the  
 sequence; information in this region is not accurate due to primer  
 degeneracy.

BASE COUNT 143 a 86 c 94 g 132 t  
 ORIGIN

```

1 gcgcaggccc acaataatgg tatttgggg ggaaatcagt tatttttac tggtagat
L1 cds ->
      -> MY11 PCR primer <-
61 actacacgta gtacaaacat gacaatatgt gctgctacaa ctcagtcctcc atctacaaca
121 tataatagta cagaataataa acaatacatg cgacatgttgg aggagtttga cttacagttt
181 atgtttcaat tatgttagtat taccttaact gctgaggtaa tggcctattt acataccatg
241 aatcctggta ttttggaaaca gtggaaacttt gggttgcgc cacccccaaa tggtacctt
301 gaagacaaat acagatatgt gcagtcacag gccattacat gtcaaaagcc tccccctgaa
361 aaggccaaagc aggaccccta tgcaaaatgg agttttttggg aggttagatct cagagaaaag
421 ttttcttagtg agttagatca atatccctt ggttag
      L1 cds ->
      -> MY09 PCR primer <-
  
```

## HPV64MY911

LOCUS HPV64MY911 458 bp ds-DNA VRL 16-OCT-1994  
DEFINITION Human papillomavirus type 64 (HPV-64), partial L1 cds, My09/My11 region.  
ACCESSION U12495  
SOURCE Human papillomavirus type 64 DNA recovered from a patient with vulvar intraepithelial neoplasia (VaIN).  
REFERENCE 1 (bases 1 to 458)  
AUTHORS Bernard,H.-U., Chan,S.-Y., Manos,M.M., Ong,C.-K., Villa,L.L., Delius,H., Peyton,C.L., Bauer,H.M., and Wheeler,C.M.  
TITLE Identification and assessment of known and novel human papillomaviruses by PCR amplification, restriction fragment length polymorphisms, nucleotide sequence, and phylogenetic algorithms  
JOURNAL J. Infect. Dis. (1994) In press  
COMMENT HPV-64 has recently been characterized and isolated from a vulvar intraepithelial neoplasia by Dr. T. Matsukura. The cloned DNA was subsequently sequenced by Dr. H. Delius over the L1 MY09/MY11 segment. HPV-64 and the several other types recently sequenced over this region by Dr. Delius were used as type-specific probes to screen DNA for novel genital HPV types. The screened DNA was obtained from four recent epidemiological studies. Primer regions are annotated in the sequence; information in this region is not accurate due to primer degeneracy.

BASE COUNT 152 a 85 c 83 g 138 t  
ORIGIN  
L1 cds ->  
1 gcacaggagc ataaacaatgg aatttgttgg cataatcaac tgtttctaac tgggttat  
-> MY11 PCR primer <-  
61 actaccagaa gtacaaactt ttctgtttgt gtaggcacac aatccacaag tacaatcca  
121 ccatatgcaa acactaattt taaggaatac ctaaggcatg cagaagagta tgacctcgag  
181 tttgtgttgc agttatgcaa aattacttta actacagatg taatgacata tatacattct  
241 atgagttcta gatatattga acagtggaaat ttgggtctta caccaccgcc atctggtaact  
301 tttagaagaaa catatagata tgtaacttca caggccattha catgtcagcg tccgcaacct  
361 ccttaaggaat ctgaggatcc atatgctaaa atgacattt gggaggtaga ccttaaagaa  
421 aagttttctg cagaatttga tcagtttcctt tttggacg  
L1 cds ->  
-> MY09 PCR primer <-

LOCUS HPVMM9 458 bp ds-DNA VRL 16-OCT-1994  
 DEFINITION Human papillomavirus isolate MM9, partial L1 cds, My09/My11  
 region.  
 ACCESSION U12491  
 SOURCE Human papillomavirus DNA recovered from a genital swab sample,  
 isolate MM9 (PAP238a).  
 REFERENCE 1 (bases 1 to 458)  
 AUTHORS Manos,M.M., Waldman,J., Zhang,T. Greer,C., Eichinger,G.,  
 Schiffmann,M., and Wheeler, C.  
 TITLE Epidemiology and partial nucleotide sequence of four novel genital  
 human papillomaviruses  
 JOURNAL J. Infect. Dis. (1994) In press  
 COMMENT MM9, also known as PAP238a, was isolated from a genital swab sample.  
 Samples were obtained from over 500 patients examined at either the  
 Shasta/Diablo planned parenthood clinic or at a private practice  
 in the state of California over the course of seventeen months.  
 Each of the samples were cervical or vulvar/intraovital in origin.  
 DNA was PCR amplified over the MY09/MY11 region and subsequently  
 sequenced if the HPV digested products yielded unique RFLP patterns.  
 This procedure resulted in the identification of four novel HPV  
 types: W13B, PAP291, PAP155, and PAP238a, which have subsequently  
 been renamed MM4, MM7, MM8, and MM9. Oligonucleotide probes over  
 the MY9/MY11 region from these viruses have been reported by  
 Hildesheim et al. (J Infect Dis 169: 235-40). These probes were  
 used to determine prevalence in different populations. Prevalence  
 for each of these viruses was similar to that seen in other  
 characterized "intermediate risk" viruses probed for in these  
 studies. In addition to anogenital sites, MM9 was identified in a  
 periungual carcinoma with multiply infected digits. It should be  
 noted that MM4 is extremely similar (90.8%) to novel HPVIS39 (U12481)  
 and MM7 is virtually identical to LVX82 (U12487). Primer regions are  
 annotated in the sequence; information in this region is not accurate  
 due to primer degeneracy.

BASE COUNT 145 a 79 c 84 g 150 t  
 ORIGIN

```

    1 gcacagggtc ataataatgg tattttgttgg cataatcaat tatttttaac tgttgttagat
L1 cds ->
    -> MY11 PCR primer <-
    61 actactagaa gcactaattt ttctgtatgt gtaggtacac aggcttagtag ctctactaca
    121 acgtatgcca actctaattt taaggaatat ttaagacatg cagaagagtt tgatttacag
    181 tttgttcttc agttatgtaa aatttagttt actactgagg taatgacata tatacattct
    241 atgaattcta ctatattgga agagtggaaat tttgggtctta ccccacccacc gtcaaggact
    301 ttagaggaaa catatagata tgtaaacatca catgcttta gttgccaacg tcctcaacct
    361 cctaaagaaa cagaggaccc atatgccaag ctatccccc gggatgtaga tcttaaggaa
    421 aagtttctg cagaattaga tcagtatccc cttggacg
                                L1 cds ->
    -> MY09 PCR primer <-
  
```